

#4

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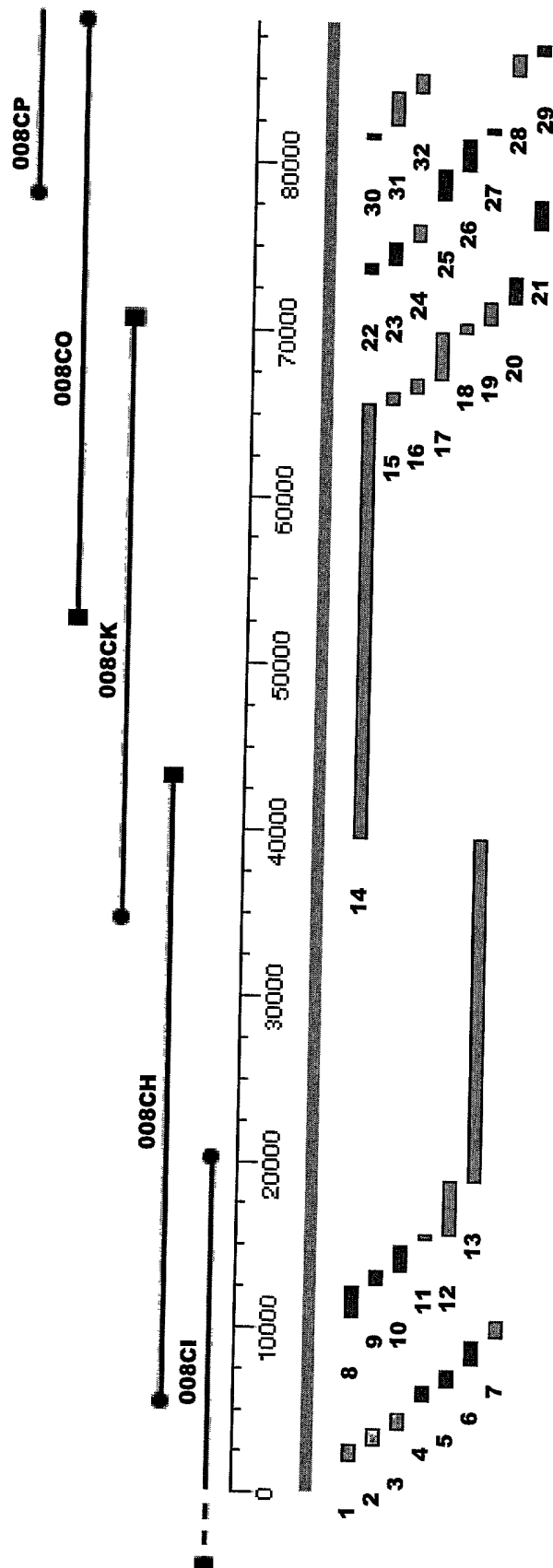
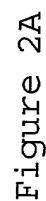


Figure 1



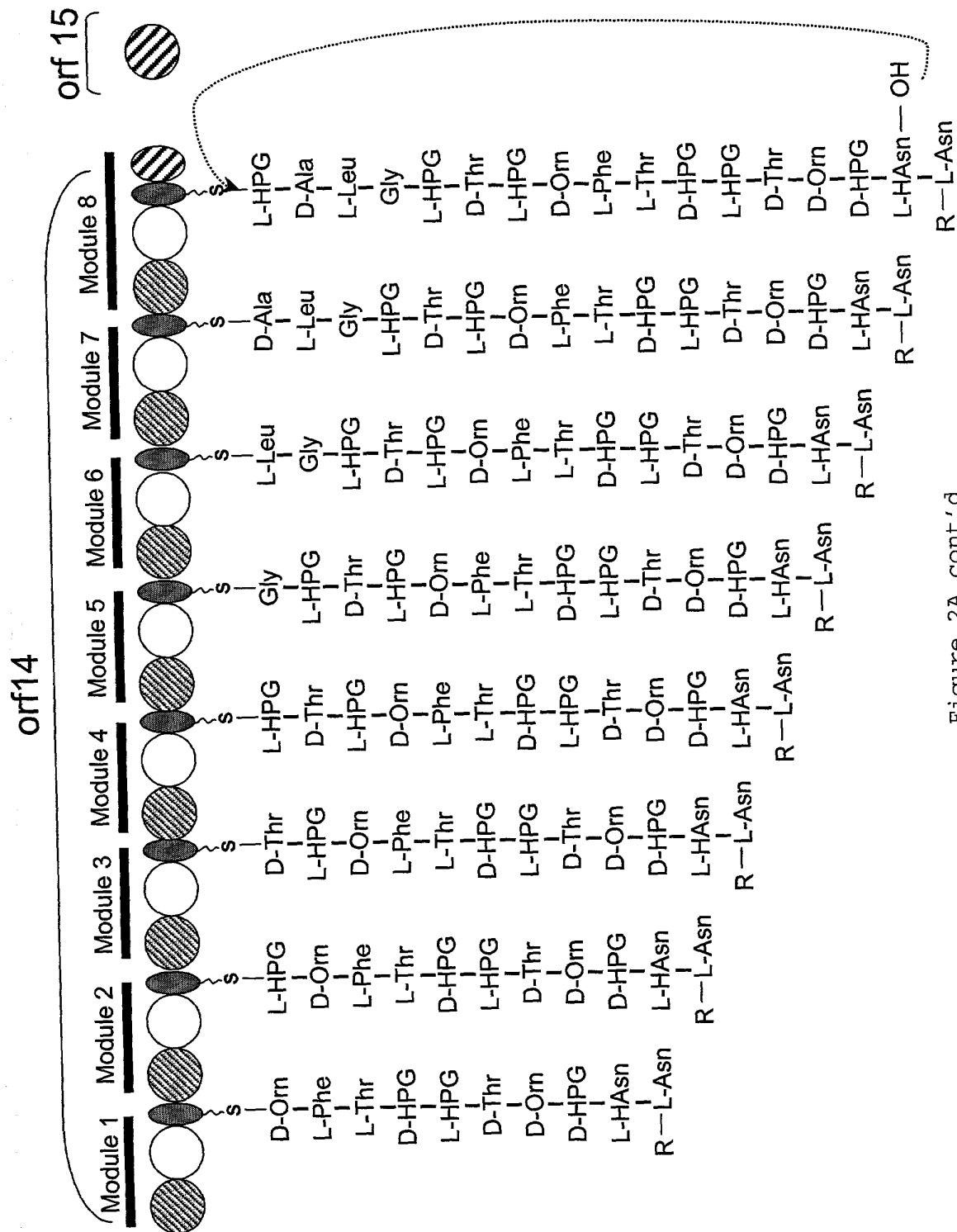
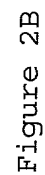
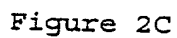


Figure 2A cont'd





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Orf12      -----ERRRLLDEWN-ATAAPSSDTVLARFEEQAARTPEAPAVVC
Orf13|M1   -----ERSRLLVEWNDTARPVVESSVPALFAKRVAATPDATAVVG
Orf13|M2   -----NATAVPAQPALVPELFTAQAARTPTWPAVLT
Orf13|M3   -----DRLLTAWNEAREPAPP-VTLPLDFDRQARRTPEAVALTA
Orf13|M4   -----EIERVVHWNDRARPVVESSVPALFAEQVAAAPDATAVVG
Orf13|M5   -----ERSRLLVEWNDTARPVVESSVPALFAEQVAAAPDATAVVG
Orf13|M7   -----TVPELVAAQVARRPGAVALRS
Orf14|M1   -----NDTAAPAPAGLVPLDFAAQAARTPDAAVAVAG
Orf14|M2   -----NDTARRVRQASVPELFAERVAAPGAPAVAA
Orf14|M3   -----EESRLMLAAGEEPAPALPEITVAALVAEQCARTPGAVAVTG
Orf14|M4   -----NETRRAVTRASVPELFAKQVAATPDAAVAVAG
Orf14|M5   -----ERRLVLTGWNDTTAAVPAVAVPELIERRAAAEPEAGAVWC
Orf14|M6   -----ERREVLRTPNATARDVAAATLPAIVGEWARTTPGATAVTA
Orf14|M7   -----EREAVLSGGNGGTAPVPVTTVPALFAEQARRTPGAVAALS
Orf14|M8   -----ERSRLLVEWNDTARPVVESSVPALFAERVAAPDATAVVG
Orf17      -----RTLTGLFAEQVAARPTAVAVSD
GrsA_Adomain MLNSSKSILIHAQNKNGTHEEEQYLFVNNNTKAEYPRDKTIHQLFEEQVSKRPNNVAIVC

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A1

A2

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Orf12      GDVTVTYAELEAGANRLARVLRLARGAGPESVVALCLPRGPEVVTGILAAWKAGAAAYLPVD
Orf13|M1   EGVSWSYRELDORSDVLARRLVAAAGVGVEPVVVALERSPEVLSAFLAVAKAGGVFVPVD
Orf13|M2   AGAEMSYAELEERSNRLARWLAGRGVGGADDRVALMMRRGPELMVAAILAVLKAGAAAYLPVD
Orf13|M3   DGVSILTYRELSERANRLIARLLTSRGIGPESLVGVVLPVSADLVVALLGVLAQAGAAAYVPVD
Orf13|M4   EGVSWSYRELDARSDALARSLVAAGVGVEPVVVALERSPEVLSAFLAVAKAGGVFVPVD
Orf13|M5   EGVSWTYRELDARSDALARSLVAAGVGVEPVVVALERSPEVLSAFLAVAKAGGVFVPVD
Orf13|M7   EDGEITYAELEARAGRLAAVLRRLRGIGPESRVAVLLPRGVEQVVAFLAVVRAGGTYPID
Orf14|M1   PDRELTYAELEDERSGRLARWLIRRGVAADTRVALVLSAELPVAILAVLKAGGAYLPID
Orf14|M2   GDLEWTYADLDARSDALARSLVAAGVTAESPVVVALERSADVLTAFLAVAKAGGVFVPVD
Orf14|M3   PDASLTAELEDERAARIARWLRRHGAGPGAACVLMERSAELVAVLLGVMRAGAAAYVPVD
Orf14|M4   EGVSWSYRELDVRSDALARSLVAAGVGIESPVVVALDRSPEVPTAFLAVAKAGGVFVPVD
Orf14|M5   GDTHLRYGELNARANRLARLLVERGAGPESIVAVCLERSADLVVTLAVLTKGAAAYLPID
Orf14|M6   ENDRITYAELEARANRLARSLIARGVGPGAVVGMLLPRSPGLVAMLAIVKAGGAYLPID
Orf14|M7   EGMSLTYADLAARVNRLARHLVSLGAGPETVVGIAMSRGLDMLVAVLAVGQAGAAAYLPVD
Orf14|M8   EGVSWSYRELDORSDVLARSLVAAGVGLESPPVVVALERSADVLTAFLAVAKAGGVFVPVD
Orf17      DRGHTTYRELEWSGRLARGRLKAGVRDGDVAVGVCLDRSAELVAVLLAVLKAGAAAYPLD
GrsA_Adomain ENEQLTYHELVNKANQLARIFIEKGIGKDTLVGIMMEKSIDLFIGILAVLKAGGAYVPID

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Orf12      TELPAERVAYLLGDSAAAVRLG--TAETLAALPDGP-----AADVDVHA
Orf13|M1   LSWPQARVDVADCAARVAVA--DRPMSGLTVVVSAGL-----GGDSAVVSA
Orf13|M2   PDLPRDRVDYLLADAAPAFVLA--ERATAPWVPVA-----GGIPVLVVDA
Orf13|M3   ADYPAERIGYILGDAGAVCVLT--VDATEAGAVPPG-----VPKLVLDH
Orf13|M4   LSWPQARIDAVVADCAARVAVA--DRPMSGLTVVPA-----GGDSAVVSG
Orf13|M5   LSWPQARVDVADCGARIAVA--DRPMSGLTVVVSAGL-----GGDSAVVSG
Orf13|M7   PAYPRDRVDYLVDAEPACLLT--VAGHRAAAPAAP-----AVVELDD
Orf14|M1   PAQPFRRIADIVADAAPALVLA--QASTADVADASPALVLAPASDGVPVGAVPVHLLDS
Orf14|M2   LSWPRARVDVADCAAWIAVA--DRPMTGLTVVPAN-----VPCLAIDD
Orf14|M3   PAYPAERIRFVVTDAACVVS--ESASAGLVDPG-----VPCLAIDD
Orf14|M4   LSWPQARVDVADCAARVAVA--DRPMTGLTVVPA-----AQRIVLGD
Orf14|M5   PGYPAGRIAYMLADARPALVTS--PAVASGDSLPDGG-----QRLLLDD
Orf14|M6   PGYPAPRLARMVEDAAPALLLA--TAGTADAVPAGP-----AAAVVLDE
Orf14|M7   PSYPDERKEFMLTDAGAAVLT--LASDADRVPVPGTP-----VRLAPES
Orf14|M8   LSWPQTRIDAVIAD-S--RPVLVLDSDVLDL-----VRLAPES
Orf17      AAYPADRIAYTVGDAGLAVVVT--TSADFPDV-DG-----VRLAPES
GrsA_Adomain IEYPKERIQLDDSQARMLLT--QKHLVHLIHNIQFN-----QQVEIFEE

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Figure 3A

A3

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Orf12      PEIARE-----SP-----SPLRLEPLPDQLAYVIYTSGSTGLSKGVGVSHGGLANYVGWAS
Orf13|M1   DLTADRAVVLPSRPVP-----GAAYRMYTSGSTGRPKGVVTTTHQNVLVDLAT---
Orf13|M2   PAVAAEVAHSGEAVTDRDRRAALRGGLHAYVIYTSGSTGRPKGVLTITHDGLANLTL-DH
Orf13|M3   PETVTALAACDTAPLGEAERAGELLPEHPAYVIYTSGSTGTPKGVLIPIHRNVVELFAATR
Orf13|M4   DQVGDSAVVLPAGPVP-----GAAYRMYTSGSTGRPKGVVTTTHQNVLVDLAT---
Orf13|M5   DLTADRAVVLPA GPVP-----GAAYRMYTSGSTGRPKGVVTTTHQNVLVDLAT---
Orf13|M7   PATAAEIADAEPEPP-----VAVRPTHSAyliYTSGSTGRPKGVVTTTHRGVAALVATQA
Orf14|M1   PAVRDEVAQC PAGAVTDADRRGVLLGGHAAyVIYTSGSTGRPKGVVVSDFANLVL-DQ
Orf14|M2   -RAGDPAVALPPRPLP-----GAAAYRMYTSGSTGRPKGVVTTTHQNVLVDLT---
Orf14|M3   P-----AAAAEPAEPGDDPGDAAGPRPDDPAYIYTSGSTGTPKGVVVSHRNVALLTATR
Orf14|M4   DAAGDPAAELPPRPLP-----GAEVYRMYTSGSTGRPKGVVTTTHQNVLVDLAT---
Orf14|M5   PDTAALDGLAGTDLVLSERRGVTHPAHPAYVIYTSGSTGRPKGVVVPHGALTNFVAAMS
Orf14|M6   PGTAAELARLDGDPIDERTHPIRPGHPAYLMFTSGSTGRPKGVLPVPHAGIDRMVR-RS
Orf14|M7   PVTAAARIAGLDPADLTADRVAPLLPAHRAyVIYTSGSTGRPKGVAVEHRTVVNLLSWAA
Orf14|M8   -----AAEADLPRVPA-----GAGVYRMYTSGSTGRPKGVVTTTHQNVLVDLAT---
Orf17      -----LAEAGDDPGIPLATPAG--PERPAYVIYTSGSTGRPKGVVVPHANVSALLDATR
GrsA_Adomain DTIKIREGTLNHLVPSK-----STDLAYVIYTSGTGPNPKGTMLEHKGISNLKVFFE

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A4

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Orf12      VLYGGLSAP---LHSSLAEDLTVTSVFVPLVCGGSVVVSAAGGGRGLASLLAAGDG--FS
Orf13|M1   -DTCWGPTPRVLFHAPHAFDASSYEIWVPLLNNGGTVVVAPQRSID-ATVCLKDLIRAHDLT
Orf13|M2   GRFGLGPGARVAQFASPGFDMFVDEWSMALLAGAALTFVPPERL-GADLAAFLAEYGV
Orf13|M3   GSFHFGEDVWSWFHSAFDFSVWELWGALHGGRVVMPFAVSRSPRDFWELLVREVRT
Orf13|M4   -DTCWGPTPRVLFHAPHAFDASSYEIWVPLLNNGGTVVVAPQRSID-ATVLRDLIRGHELT
Orf13|M5   -DTCWGPTPRVLFHAPHAFDASSYEIWVPLLNNGGTVVVAPRRSID-ATVLRDLIGAEHLE
Orf13|M7   ERLAVTGESRVLQFASVGFDASTWEMVMALCAGATLVVAPADDLLPGPALAATLSGHAVT
Orf14|M1   RRLGIGPGSRVAQFASPGFDMFVDEWSMALLAGAALVIVPPERL-GADLAAFLTERGVT
Orf14|M2   -DRCWGPTPRVLFHAPHAFDASSFELWVPLLTGGTVVAPGESID-TGVLRLQIRAEHLE
Orf14|M3   PLFGFAGDEVWSWFHSAFDFSVWELWGALHGGRVVVPYAVSRSPRDFWELLVREGVT
Orf14|M4   -DTCWGPTPRVLFHAPHAFDASSYEIWVPLLNNGGTVVVAPGRSID-AAVLGELIRAEHLE
Orf14|M5   DRALAGAGDRLLAVTTVAFDIHVLELYVPLVGGAGVVAEDAVVRDPAAVAALLDRHAVT
Orf14|M6   TCIQLAPDDVPLHLSSVSFDAATEIWGALLNGATLAVAPAETLS-VAELRAFLADRAGT
Orf14|M7   GRFGGADFARTLAATSLNFDVSVSEIFGPLVSGGSIEIVTDLALADPASPAAWEA----S
Orf14|M8   -DTCWGSTPRVLFHAPHAFDASSYEIWVPLLNNGGTVVVAPRRSID-ATVLRDLVRGHELT
Orf17      EEYALGPGDVWTFHSAFDFSVWELWGCLLTGGHLVVVPYVWSRSPQFHDLLAERGVT
GrsA_Adomain NSLNVTEDKDRIGQFASISFDASVWEMFMALLTGASLYIILKDTINDFVKFEQYINQKET

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A5

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Orf12      LRVVPGHLRLLAELVPAGEMA AVG---SLVAGGEVLAGGDVREWLSRVPGS--VVVNE
Orf13|M1   HVEVTA---GLLRVL---DPSCFAG--LTEVLTGGDAVSAEAVRRVKDANPGL--RVROL
Orf13|M2   HATLPP---AVVGTIPDGVLPSSF-----VLVGGDVLPGLDARR--WLRDGR--VLNS
Orf13|M3   VLSQTP---SAFYQLAAAA-DDTPD-ALRVVFGGEALDPGRLAGWRERRPDG-PRLVNM
Orf13|M4   HVEVTA---GLLRVL---DPSCFAG--LTEVLTGGDAVSAEAVRRVREANPGL--RVROL
Orf13|M5   HVEVTA---GLLRVL---DPSCFAG--LTEVLTGGDAVSAEAVRRVKDANPGL--RVROL
Orf13|M7   HATLPP---AVLAASAPGDLAPLA-----VLVSAGEALGPDVLR---QFAPGR--ALVNA
Orf14|M1   HATLPP---AVVATLPEESLPRSF-----VLIDGGDALPDDLARR--WLRDGR--WLGNS
Orf14|M2   HVEVTA---GLLRVLAE-DPSCFAG--LTEVLTGGDVVPAEAVRRVLDANPGV--RVROL
Orf14|M3   VLSQTP---SAFAQLMAAAGDDDRD-ALRFVFGGEALDPGRLAGWLARRPDK-PRLVNM
Orf14|M4   HVEVTA---GLLRVL---DPSCFAG--LTEVLTGGDAVSAEAVRRVMEANPGL--RVROL
Orf14|M5   IVQATP---ALWQALLAGHADAVRD---VRLVGGGEALPPALAG--RMAAAGR--GVTNL
Orf14|M6   KLELT---GLLHEVIDADVTALAG--LKAVYTCGGDVLSPAHCRSLDRVPGI--ELVNA
Orf14|M7   LVSGVP---SAFSRVLDRGDIAART---RSVVLAGEALTADVNNATRAALPGV--RVANL
Orf14|M8   HVEVTA---GLLRVL---DPSCFAG--LTEVLTGGDAVSAEAVRRVKEANPGL--RVROL
Orf17      VLNQTP---SSFTQLVAADRGAEERDLAVRLVIFGGEPLDARTVLPWLDLRRPEARCLVNM
GrsA_Adomain VITLPP---TYVVHLDPERILSIQT-----LITAGSATSPSLVNKWEKVT-----YINA

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Figure 3A cont'd

	A5	A6
Orf12	YGPTEVTVGCSVFSVAAGDVVGD--VVPVGRPVANTRLFVLDDEGLRPVPAGVAG	GELYVAG
Orf13 M1	YGPTEVTLCAQHLLD-DG-----VPIGRPLDNTRVYVLDLLQPVVPGVT	GELYVAG
Orf13 M2	YGPTEVTVNAATWR-AEAGDWGS--VAPIGTFVPNLRAVYVLDGWLRPVPVGA	GELYVSG
Orf13 M3	YGITETTVHVTHQDLAPAD-TTG--S-PIGRGIPGLSVYVLDALRPVPPGVA	GEVYVAG
Orf13 M4	YGPTEVTLCAQHLLV-DG-----VPIGRPLDNTRVYVLDLLQPVVPGVT	GELYVAG
Orf13 M5	YGPTEVTLCAQHLLD-DG-----VPIGRPLDNTRVYVLDLLRPVPTGVV	GELYVAG
Orf13 M7	YGPTEVTVCATASAPLGPEDPPH-----IGAPVADSRVYVLDLALTPVPPGVT	GELYVSG
Orf14 M1	YGPTEVTVNAATWR-CEPGTWEG--ATPIGRPVANLRAVYVLDGRLRPVPVGV	GELYVSG
Orf14 M2	YGPTEVTLCAQHVVREPSV-----LPIGRPLDNTRVYVLDGLLQPVVPGVT	GELYIAG
Orf14 M3	YGITETTVHTTYQHIAFG--TTG--S-VIGRGLPGFGLYVLDALRPVPAGV	GEVYARG
Orf14 M4	YGPTEVTLCAQHLLD-DG-----VPIGRPLDNTRVYVLDLLQPVVPGVT	GELYVAG
Orf14 M5	YGPTEVTVWATVADLGA-SPAG---PVPIGTPLRNTRAFVLDLALRPVPPGV	GELYLAG
Orf14 M6	YGPTEVTVITLHR-VREPDLTAGTVPIGVPISTRVYVLDLALRPVPVGV	GELYTSG
Orf14 M7	YGPTEATVYSTAWHTDR-DVTGG--AAPIGRPVTNTRAYVLDLRLTPVPPGV	GELYLAG
Orf14 M8	YGPTEVTLCAQHLLD-DG-----VPIGRPLDNTRVYVLDLLRPVPTGVV	GELYVAG
Orf17	FGITETTVHVTAVDVTRAAALAG--SRVGRPLPGWAVRVLDGQRREVPPGV	GEIYVGG
GrsA_Adomain	YGPTEVTVCATVWATKETIGHS---VPIGAPIQNTQIYIVDENLQKSVGEA	GELCIGG

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	A6	A7	A8
Orf12	SQVARGYVGRSGLTASRFVACPFV-GGERMYRTGDVVRLAG-GDLVFFVGRVDEQVKIRGY		
Orf13 M1	AGVARGYAGMPGLTAERFVADPFNT-GGRLYRTGDLVRWTDGVLHFAGRADDQVKIRGY		
Orf13 M2	AGLARGYINRAGLTAERFVACPFEP-GERMYRTGDVVRWTAEGRLVFAGRSDDQVKIRGF		
Orf13 M3	RQLARAYIGRAALTGTREVFACPFEPAGERMYRTGDRARWSR-GRLOFAGRTDDQVKIRGF		
Orf13 M4	AGLARGYAGMPGLTAERFVADPFVSV-GGRLYRTGDLVRWTDGVLHFAGRADDQVKIRGY		
Orf13 M5	SGLARGYAGMPGLTAERFVADPFNT-GGRLYRTGDLVRWADDGVLHFAGRADDQVKIRGY		
Orf13 M7	ASLARGYAGRAALTAERFVACPFAP-GERMYRTGDRARWDAAGRLTFAGRADDQVKIRGF		
Orf14 M1	AGLARGYINRAGLTAGSFVACPFEP-GERMYRTGDIVRWDARGRLVYAGRADDQAKIRGF		
Orf14 M2	AGVARGYADMPGTTAERFVADPFNT-GGRLYRTGDLVRWTGEGELVFAGRADDQVKIRGY		
Orf14 M3	PQVARGYIGRPLTAERFVACPFAP-GERMYRTGDVARWTADGRLVFAGRSDDQIKIRGF		
Orf14 M4	AGLARGYAGMPGLTAERFVADPFSS-GGRLYRTGDLVRWTDGVLVFAGRADDQVKIRGY		
Orf14 M5	DQLARGYHGRAGLTAERFVADPFV-RGERMYRTGDRVRWTRGGSLEFLGRVDDQVKIRGF		
Orf14 M6	IGLAHGYAGRPAPTAERFVACPFAP-GERMYRTGDLVRWTADGRLVFAGRADNQVKIRGF		
Orf14 M7	AQLARGYIGRPLTGGERFVACPFEPGGERMYRTGDRVRWNADGDLVFAGRADDQVKIRGF		
Orf14 M8	SGLARGYAGMPGLTAERFVADPFVSV-GGRLYRTGDLVRWTDGVLHFAGRADDQVKIRGY		
Orf17	AGVAIGYINRPELTAERFVVTG---PDGRRWYRSRGRLLPDGTLEHLGRLLDQVKIRGF		
GrsA_Adomain	EGLARGYWKREPLTSQKFVDNPFVPE-GEKLYKTGDQARWLSGDNIEYLGRIDNQVKIRGH		

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	A8	A9
Orf12	RVEPDEVRLVVAGHPRVAGAAVVARPDVAGE---RQLVAYVVAAGEPAG---LAESVRAH	
Orf13 M1	RVEPGEVEAVLAQHDPVSVQAVVREDTPGD---KRLVAYVVGG-----DIEAY	
Orf13 M2	RIEPGEVEAVLAAGPGVSVQAAVIVREDVPGD---KRLVAYVVGG---D---VEALRSY	
Orf13 M3	RIEPGEVQAVVAHPEIAAAVAVVREDVPGD---PRLTAYVVPAGPRTAPAAVAETVRRF	
Orf13 M4	RVEPGEVEAVLAQHDPVSVQAVVREDTPGD---KRLVAYVVGG-----DVEAY	
Orf13 M5	RVEPGEVEAVLAQHDPVSVQAVVREDTPGD---KRLVAYVVGG-----DVEAY	
Orf13 M7	RVEPGEVAAVLGEHPAVARAAVVARTDGPQG---ARLVAYLVAAADP---AGPDLAAAVRAY	
Orf14 M1	RVEPGEVEAVLAAGPGVNQVAVIVREDVPGD---KRLVAYVVGG---D---VETLRSY	
Orf14 M2	RVEPGEVEAVLAALPGVSVQAAVIVREDVPGD---KRLVAYLVAAPE-----TVEAARAH	
Orf14 M3	RIEPGEVEAVLAAGPGVSVQAAVIVREDVPGD---KRLVAYVVGG-----DAETLRSH	
Orf14 M4	RVEPGEVEAVLAHDPVAVQAVVREDTPGD---KRLVAYVVGG-----DVEAY	
Orf14 M5	RIELGEVEAALAAFGPVARAAAIVREDVPGD---RRLVGYVVPVAAAGEPE---PDPAAVRAH	
Orf14 M6	RVEPGELETVLSGHPAVARAVALAREDTPGA---KRLVAYVVPARPDEDGDALAESVRAH	
Orf14 M7	RIEPGEVQAVVARQAGVARAVVLARS DSPGD---ARLVAYVVPADRDADRRALAATVRS	
Orf14 M8	RVEPGEVEAVLAQHDPVSVQAVVREDAPGD---KRLVAYVVGG-----DVEAY	
Orf17	RIELDEIRGVLTECAGVAAAIVIRSTPDDPATARLDAYVVAEAG-----ATPPVAEH	
GrsA_Adomain	RVELEEVESEILLKHYISSETAVSVHKDHQEQ---PYLCAYFVSEKHIP-----LEQLRQF	

\*: \* \* : : : . . . : . \* : \* \*

Figure 3A cont'd (2)



	A10
Orf12	VAERLPEYMPVPAVVTLDEIPLTVNGKVDRAALPEP-----
Orf13 M1	GQERLPGYMPVSAFVHLDALPLTSNQKVDRAALPAPSMESG-----
Orf13 M2	AQQRLPGYMPVSAFVELDRLPLTVNGKLDRAALPVVDLARG-----
Orf13 M3	AADRLPAYMLPSAVVVLDALPLTDHGKLDRAALPAPQHT-----
Orf13 M4	AQERLPGYLVPSAFVHLDALPLTSNQKVDRAALPAPSVESGV-----
Orf13 M5	AQERLPGYMPVSAFVQLDALPLTSNQKVDRAALPAPSMESG-----
Orf13 M7	AAATLPAHLLPAAFVPLDRLPLTVNGKLDRAALPEPETGAG-----
Orf14 M1	AQQRLPGYLVPSAIVALAELPLTESAKVDRRALPVVD-----
Orf14 M2	AEQRLPSYLVPSAFVQLDALPLTGNQKVDRAALPAP-----
Orf14 M3	AQQRLPGYLVPSAFVELDRLPLTVNGKLDRAALPVVD-----
Orf14 M4	AQERLPGYLVPSAFVHLDALPLTSNQKVDRAALPAPSVESG-----
Orf14 M5	VAAQLPAYMPVSAVVVLPDLPLTANGKLDRAALPAPDYGAASAGRAPADE--
Orf14 M6	AARQVPDYLMPAATVVLPDLPLTSSGKVDRAALPAPDVPGG-----
Orf14 M7	TARELPAYLVPAVVVLDLPLTVNGKLDRAALPAPGL-----
Orf14 M8	AQERLPGYMPVSAFVHLEALPLTANGKVDRAALPAPE-----
Orf17	AARMLPAYMCPTFTFLDALPMTENGKVDRAALPEP-----
GrsA_Adomain	SSEELPTYMIPSYFIQLDKMPLTSNGKIDRKQLPEPDLTFGMRVDYEAPRNE
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Figure 3A cont' d (3)

	235	236	239	278	299	301	322	330	
Orf13 M1 HPG	D	A	Y	H	L	G	L	L	HPG
Orf13 M4 HPG	D	A	Y	H	L	G	L	L	
Orf13 M5 HPG	D	A	Y	H	L	G	L	L	
Orf14 M2 HPG	D	A	F	H	L	G	L	L	
Orf14 M4 HPG	D	A	Y	H	L	G	L	L	
Orf14 M8 HPG	D	A	Y	H	L	G	L	L	
emb CAB38518.1 Cda1 M6 HPG	D	V	Y	H	L	G	L	L	
emb CAA11795.1 CepB M2 HPG	D	A	V	H	L	G	L	L	Thr
emb CAA11795.1 CepB M1 HPG	D	I	F	H	L	G	L	L	
Orf13 M3 Thr	D	F	W	S	V	G	M	V	
Orf14 M3 Thr	D	F	W	S	V	G	M	V	
Orf17 M1 Thr	D	F	W	N	I	G	M	V	
gb AAC38442.1 AcmB M1 Thr	D	F	W	N	V	G	M	V	
emb CAB38518.1 Cda1 M2 Thr	D	F	W	N	V	G	M	V	
emb CAA09819.1 FenD M2 Thr	D	F	W	N	I	G	M	V	Orn
Orf13 M2 Orn	D	M	D	T	D	G	S	V	
Orf14 M1 Orn	D	M	D	T	D	G	S	V	
gb AAC06347.1 BacB M1 Lys	D	A	E	S	I	G	S	V	
gb AAC82550.1 FxbC M1 5hOrn	D	M	E	N	L	G	L	I	
gb AAC82550.1 FxbC M3 5hOrn	D	M	E	N	L	G	L	I	Asn
Orf12 M1 Asn	D	L	T	K	V	G	E	V	
emb CAB38517.1 Cda2 M3 Asn	D	L	T	K	V	G	E	V	
gb AAC06348.1 BacC M5 Asn	D	L	T	K	I	G	E	V	
gb AAC45930.1 TycC M1 Asn	D	L	T	K	I	G	E	V	Phe
Orf13 M7 Phe	D	A	W	T	V	A	A	V	
emb CAA33603.1 GrsA M1 Phe	D	A	W	T	I	A	A	I	
gb AAC45929.1 TycB M3 Phe	D	A	W	T	I	A	G	V	
gb AAC06348.1 BacC M2 Phe	D	A	F	T	V	A	A	V	Gly
Orf14 M5 Gly	D	I	L	Q	L	G	L	V	
emb CAB38517.1 Cda2 M2 Gly	D	I	L	Q	L	G	L	I	
emb CAB15186.1 DhbF M1 Gly	D	I	L	Q	L	G	L	I	
gb AAF17280.1 NosC M2 Gly	D	I	L	Q	L	G	L	I	Leu
Orf14 M6 Leu	D	A	F	F	Y	G	A	T	
emb CAA82227.1 CssA M2 Leu	D	A	W	L	Y	G	A	V	
emb CAA82227.1 CssA M3 Leu	D	A	W	L	Y	G	A	V	
gb AAC06346.1 BacA M3 Leu	D	A	W	F	L	G	N	V	(Ala)
Orf14 M7 (Ala)	D	V	F	S	V	A	I	V	
gb AAC06348.1 BacC M2 Phe	D	A	F	T	V	A	A	V	
gb AAC83656.1 PchE M1 Cys	D	L	F	N	L	S	L	I	
emb CAA82227.1 CssA M11 Ala	D	V	F	I	Y	A	A	I	

Figure 3B

Orf26  
gb|AAB52538.1|acyl\_CoA\_L|Mb  
emb|CAB05426.1|fadD29|Mt  
gb|AAG02359.1|blmVI|M1|Sv  
gb|AAC44128.1|safB|M1|Mx  
gb|AAF08795.1|MycA|M1|Bs

-----MVIDAATQPTVPDAFRAQ  
-----MAMSVRSLPAALRAC  
MKTNSSFHAAGEVATQPAWGTGEQAAQPLNGSTSRFAMSESSLADLLQKA  
-----MSRPAGIVDIARRH  
-----MACRPDSLHASAVTSRRRMRHTLVELLQER  
-----MYTSQFQTLVDVIRNR  
:  
:

Orf26  
gb|AAB52538.1|acyl\_CoA\_L|Mb  
emb|CAB05426.1|fadD29|Mt  
gb|AAG02359.1|blmVI|M1|Sv  
gb|AAC44128.1|safB|M1|Mx  
gb|AAF08795.1|MycA|M1|Bs

AIARPGEPALVVLPG--DPDAEPVTLTYAELDRRAAARAAWLAARFPAGE  
ACLQPHDPAFTFMDYEQDWDGVAITLTWSQLYRRTLNVARELSRCGSTGD  
ASQYPNRAAYKFIDYDTPAGFTETVTWQVHRRAMIVAEELWIYASSGD  
AERTPARPAYAFLP---DGETESVRFSFADIDRRARAFAVAVLQDRGLAGE  
ALSEPRHEAFTFLG---EAGVPAVRVDYSSMDVLARAIAARLQADGRVGE  
SNIS--DRGIRFIE---SDKIETFSYRQLFDEAQGFLGYLQHIGIQPK  
:  
: . : . : . : \*

### AL1

Orf26  
gb|AAB52538.1|acyl\_CoA\_L|Mb  
emb|CAB05426.1|fadD29|Mt  
gb|AAG02359.1|blmVI|M1|Sv  
gb|AAC44128.1|safB|M1|Mx  
gb|AAF08795.1|MycA|M1|Bs

R-ILIALPTGAEEFVELYLACLYAGLVAVPAPPPGGS--SGASERTVGIAA  
R-VVISAPQGLEYYVVAFLGALQAGRIAVPLSVPPQG---VTDERSDSVLS  
R-VAILAPQGLEYYIAFMGVLAQGLIAVPLVPVQFG---IHDERISSALR  
R-VLVAYSPGPEYVQAFGLCLYAGVVAVPQDEPR-S--GPSAERLAGIRA  
R-ALLLYAPGPEYVAAFFGCLYAGVVAVPVVPPDTARLERSLLRLRTVAR  
QEIVFQIQENKSEFVVAFWACLLGGMIPVPV\*  
:  
: . : . : . : \*

Orf26  
gb|AAB52538.1|acyl\_CoA\_L|Mb  
emb|CAB05426.1|fadD29|Mt  
gb|AAG02359.1|blmVI|M1|Sv  
gb|AAC44128.1|safB|M1|Mx  
gb|AAF08795.1|MycA|M1|Bs

DCSPALAVVN---ADDAAPLTA-----VLRERGLSGLPVGALPPLAAE  
DSSPVAILTTS---SAVDDVVQ---HVARRPGESPPIIEVDLLDLDPAN  
DSAPSIILTTS---SVIDEVTYAPHACAAQGSAPIVVAVDALDLSSSR  
DARPALALTA---GAPEAGLA-----GLATLDVAGVPDASAAG  
DSRASVVLTTSFLLQGLAGAMFEL-----APELGELSWVATDGTIALEAG  
NPFLLASETVLDKMKKFAADHD-----LQDFHHQLIEKSDIIQDRIYD  
:  
:

### AL2

Orf26  
gb|AAB52538.1|acyl\_CoA\_L|Mb  
emb|CAB05426.1|fadD29|Mt  
gb|AAG02359.1|blmVI|M1|Sv  
gb|AAC44128.1|safB|M1|Mx  
gb|AAF08795.1|MycA|M1|Bs

AIRPPRGRPRDSLAVLQYSSGSTGSPKGVMLSHRAVLANLRAFRDSSGHN  
GYTFKEDE-YPSTAYLQYTSGSTRTTPAGVVMVSHQNVVRNFEQLMSGYFAD  
ALDPTRFE-RPSTAYLQYTSGSTRTAPAGVVLVSHKNVITNCVQLMSDYIGD  
AWTDPVAG-PDALAFQYTSGSTRRPRGMVGHGNLANERCIAAACGHD  
AWKPPGLS-GDSVAFQYTSGSTADPKGVVLTHRNLMHNLVSIHERFQLN  
HPASQYEPEADELAFIQFSSGSTGDPKGVMLTHHNLHNTCAIRNALID  
\* : : : \* \* \* : \* : \* :  
:

### AL3

Orf26  
gb|AAB52538.1|acyl\_CoA\_L|Mb  
emb|CAB05426.1|fadD29|Mt  
gb|AAG02359.1|blmVI|M1|Sv  
gb|AAC44128.1|safB|M1|Mx  
gb|AAF08795.1|MycA|M1|Bs

SDDVF-----GSWLPLHDMGLFAMLTAGLLNGAGVVLMSPTAFVRRPA  
TDGIPPPNSALVSWLPPFYHDMGLVIGICAPILGGYPAVLTSPVSFLQSPA  
SEKVP---STFVSWLPPFYHDMGLMGIILPMINQDTAVLMSPMFLQSPA  
RDSTF-----VGWAPFFHDMGLVANLLQPLYLGLSVLMPMAFLQSPA  
RGSRG-----VIWLPPFYHDMGLIGVLTPIFGGLPVDLMSPLSFLQEPL  
LKDTL-----LSWMPLTHDMGLIACHLVPALAGINQNLMPTFLFIRPI  
\* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \*  
\* . . : : \*

Figure 3C

AL4

Orf26  
gb|AAB52538.1|acyl\_CoA\_L|Mb  
emb|CAB05426.1|fadD29|Mt  
gb|AAG02359.1|blmVI|M1|Sv  
gb|AAC44128.1|safB|M1|Mx  
gb|AAF08795.1|MycA|M1|Bs

DWLRMMDRYRVTI SAAPNFAYDLCVRAVRDEQIAGLDLSRIRTLYNGSEP  
RWMHLMASDFHAF SAAPNFAFELAAARRTDDDDMAGRDLGNILTLISGSE  
RWMQLLAKHRAQI SSAPNFGFELAVRRTSDDDMAGLDLGHVRTIVTGAER  
RWLRAVSRYRAHT SGGPNFAYDLCVDRVGEDERAGLDLSGWKVAYNGAEP  
RWLKTLSERRGTC SGGPNFAYELCVRKISDEQKAGLDLSSWELAFCGAEP  
LWMKKAHEHKASI LSSPNFGYNYFLKFLKDNKSYDWDLSHIRVIANGAEP  
\*:: ..\*\*\*::: ... \*\*.\*

AL5

Orf26  
gb|AAB52538.1|acyl\_CoA\_L|Mb  
emb|CAB05426.1|fadD29|Mt  
gb|AAG02359.1|blmVI|M1|Sv  
gb|AAC44128.1|safB|M1|Mx  
gb|AAF08795.1|MycA|M1|Bs

VNPATVRAFTERFAPFGLHTHAVN PCYGMAEFTAYVSTKVFEAPAVFLPA  
VQAATIKRFADRFAFNLQERVIRPSYGLAEATVYVATSKPGQPETVDF  
VNVATLRRFATERFAPFNLSETAIRPSYGLAEATVYVATAGPGRAPKSVCF  
VRADTLRRFTDRFAPHGFTPGAHFPTYGLAEATLVATGPKGVPPRTLT  
IRPDTLEAFSKAFEP CGFRREAFYPCYGLAEGTLIVTGVSKGRAARVEHF  
ILPELCDEFLTRCAAFNMKRSAIL NVYGLAEASVGATFSNIGERFVPVYL  
: \* .. \*\*.\*: :

Orf26  
gb|AAB52538.1|acyl\_CoA\_L|Mb  
emb|CAB05426.1|fadD29|Mt  
gb|AAG02359.1|blmVI|M1|Sv  
gb|AAC44128.1|safB|M1|Mx  
gb|AAF08795.1|MycA|M1|Bs

DPRALEDAASPALRPADP-AAAREIP---GVGRV-PDFEVLIVDPDGLRP  
DTESLSAGH---AKPCAGGG-ATSLIS----YMLPRSPIVIRIVSDTCTIE  
DYQQLSVGQ---AKRAENGSEGANLVS----YGAPRASTVRIVDPETRME  
DRAALRAGR---LRPAGPGEGLELV---GNGTAGLDTTLRIVDPATARE  
QREALEAHR---AVAASSPGEAARDTVRHVSCGTVPVDEQILVDPETRTA  
HRDHLNLGE---RAVEVSKEDQNCASFVEVGKPIDYQCIRICN-EANEG  
\* : : :

AL6

Orf26  
gb|AAB52538.1|acyl\_CoA\_L|Mb  
emb|CAB05426.1|fadD29|Mt  
gb|AAG02359.1|blmVI|M1|Sv  
gb|AAC44128.1|safB|M1|Mx  
gb|AAF08795.1|MycA|M1|Bs

LP EGRVGEIWL RGP GAGAGYWGRT ELNPGIFDAR PAGDG---QDGGWVRT  
CPDGT VGEI WVHGD NVGNGYWK PDESERTFGGKI VTPSPGTPEGFWLRT  
NPAGTVGEI WVQGD NVGLGYWRNPQQT EATFRARLVTPSPGTSEGFWLRT  
CPPGEVGEVWVRGPGVARGYFGRPRESAPLLAARLP GG-----EGFYLRT  
LPPGHIGE I WVRGSPV AQGYWLRPEETARTFQARLAGG---TEAFWLRT  
LEDGFIGHIQIKGENVTQGYNNPESTNRALTP-----DGWVKT  
\* :\*.::\* .. \*\*.\*: :

AL6

AL7

Orf26  
gb|AAB52538.1|acyl\_CoA\_L|Mb  
emb|CAB05426.1|fadD29|Mt  
gb|AAG02359.1|blmVI|M1|Sv  
gb|AAC44128.1|safB|M1|Mx  
gb|AAF08795.1|MycA|M1|Bs

GDLGALTGGELFLT SRLKELLIVHGRNLAPHDLREAREAAHDAVDHQIGA  
GDSGFVTDGKMFIT GRIKDLLIVYGRNHSPDDIETIQEITRGR----CA  
GDLGVIFEGELFIT GRIKELLVVDGANHY PEDIEATI QEITGGR----VV  
GDLGALHDGELFLT GRHKDLIVIRGQNHHPHDLERTAEQAHPALRP TCAA  
GDLGFLHDGELFVS GRRKDLLVIRGRNYYPQDLELTVERSHPALRPGCAA  
GDLGFIRKGNLVVT GREKDII FVNGKNVYPHDIERVAIELEDIDLGRVA  
\*\*.\*: :\*.::\* \*\*.\*: :\*

Orf26  
gb|AAB52538.1|acyl\_CoA\_L|Mb  
emb|CAB05426.1|fadD29|Mt  
gb|AAG02359.1|blmVI|M1|Sv  
gb|AAC44128.1|safB|M1|Mx  
gb|AAF08795.1|MycA|M1|Bs

AFGVPA P--DERIVLVQEVHPRTPLDLPR-----VASAVSRLTVSFGV  
AISVPGDRRTEKLVAI IELKKRGDSQDAMARLGAIKREVTSSSSHGL  
AIAVPDDR-TEKLV TIIELMKRGRTDEEEKNRLRTVKREVASAISRSRHL  
AFAVPGDG-AERLVLVCELT SYRAVDPAA-----VAEAVRAALAAHRGV  
VFSVSVGA-SEEVVVQEVDRRYPGGDWD-----VIAAIRRDI SEQHAL  
ACGVYDQETRSREIVLFAVYKKSADRFAP-----LVKDIKKHLYQRGGW  
.\* : : : : : : : :

Figure 3C cont'd

## Orf26

```

PVRNVLLVRRGT|VRRTTSGKIRRTAVRERFLAGGITALHAELEPALRPVQ
SVADLLVLPAGS|IPTTSGKVRRGACVEQYRQDQFARLDA-----
RVADVVMVAPGS|IPVTTSGKVRG|SASVERYLHFEFSRLDMA-----
APHTLVLLRRAG|PKPTSGKVRRG|HCHRTAYLDGTLPLVHTAVRLP-----
RVHAVVLKSGS|LLKPTSSGKVQRG|ATREAYLEGGQLDTSADAAQEPVGE-
SIKEILPR--|KLPKTSSGKVRYELAEQYESGKFALFESTKIKEFLEG--
               :   :   *   :   *   :   :   :   :

```

## Orf26

gb|AAB52538.1|acyl\_CoA\_L|Mb  
emb|CAB05426.1|fadD29|Mt  
gb|AAG02359.1|blmVI|M1|Sv  
gb|AAC44128.1|safB|M1|Mx  
gb|AAF08795.1|MycA|M1|Bs

AGAGR

1000	1000	1000	1000	1000
1000	1000	1000	1000	1000
1000	1000	1000	1000	1000
1000	1000	1000	1000	1000
1000	1000	1000	1000	1000

13 / 16

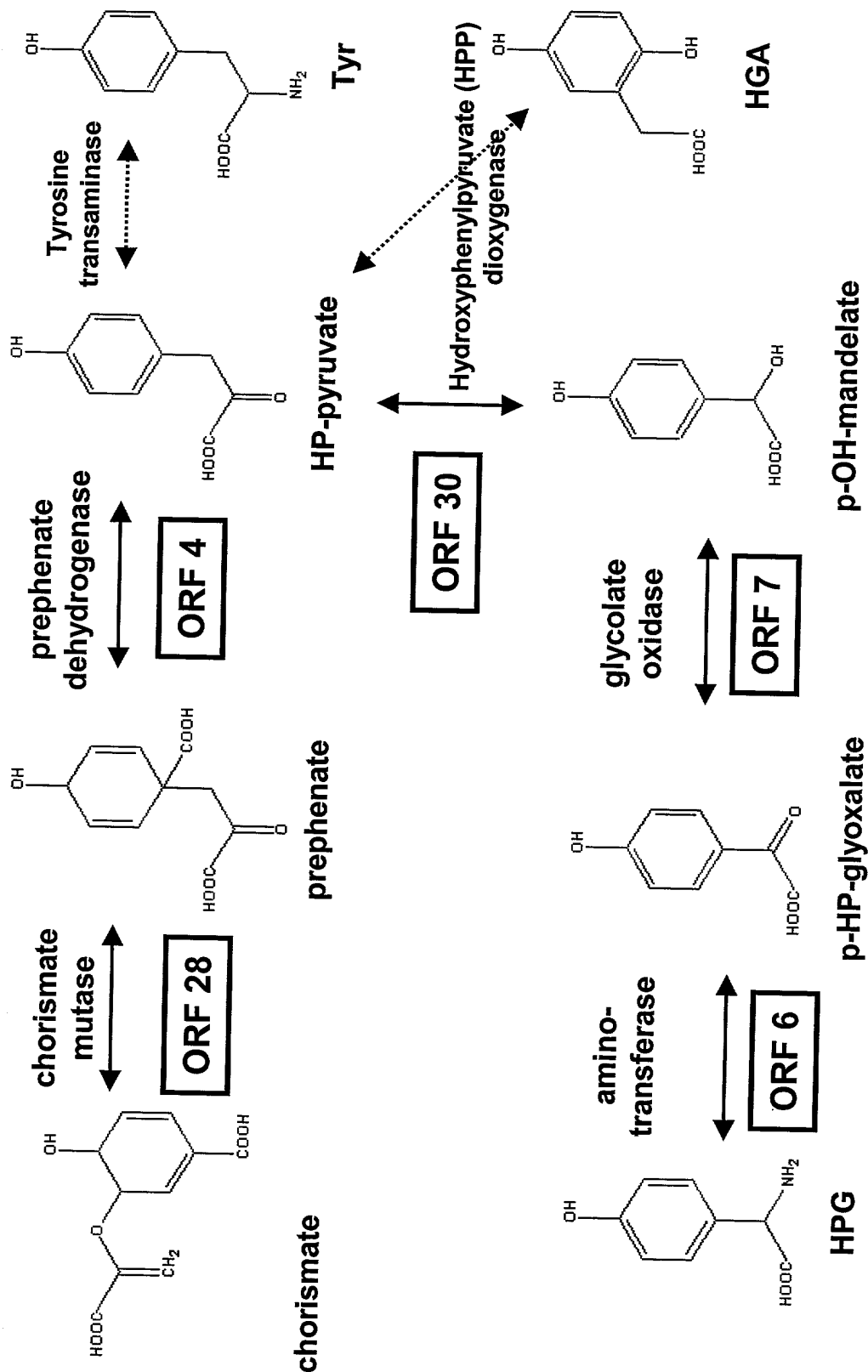


Figure 4

```

LVEDDDGAALIDTGFTAPAAKALLRLLKDG-- GKKIDAIILTHAHADHIGGVPELLER
LVQTPDGAVLLDGGMPQMASHLLDNMKARGVTPRDLRLILLSAHADHAGPVAELKRR
VMQTEQAAVVTDG-FISTDNRHGDRYTLDDL- PDHIDLVLITHGHQDHIVLETLQLR
:::  ::*: *   :   :   .   .   .   .   .   .   .   .   .   .   .   .   .   .

```

Figure 5A

```
DPE--RFLDEN- GKFKKSYAFLPAGAGPRNCLGERLARMELFLFLATLLQRFEE
DPVLYRYIRDHVGQVD----- MAFI-G-MECDGAPLNWLYKGLLTKPVNKMSAS
**  *::: *::: : * : * : * : * : * : * : * : * : * : * : *
```

Figure 5B

[illegible]

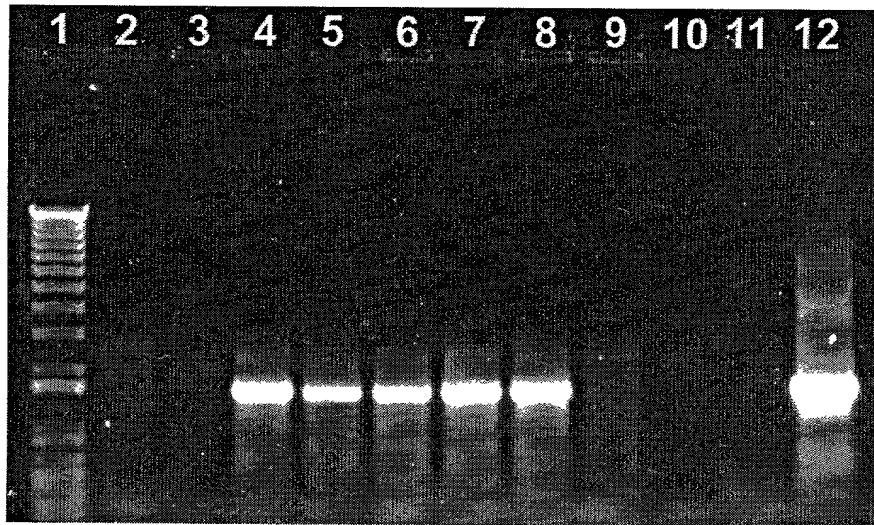


Figure 6

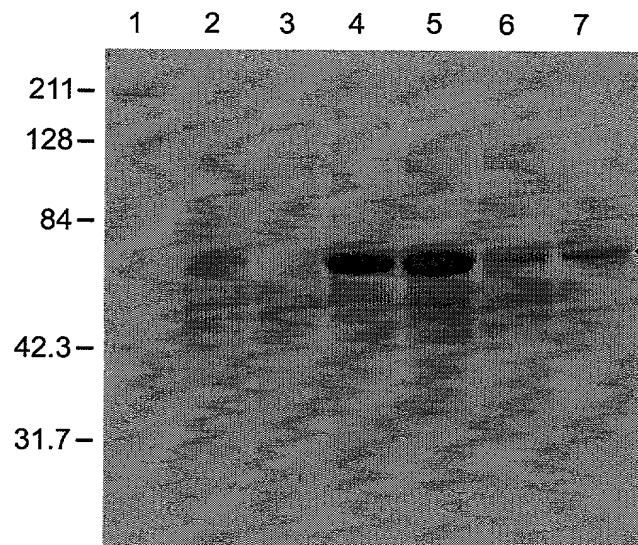


Figure 7